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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=4; day=23; hr=10; min=48; sec=52; ms=992;]

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Application No: 10577008 Version No: 2.0

Input Set:

Output Set:

Started: 2009-04-10 15:09:39.405
Finished: 2009-04-10 15:09:40.968
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 563 ms
Total Warnings: 17
Total Errors: 0
No. of SeqIDs Defined: 17
Actual SeqID Count: 17

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SEQUENCE LISTING

<110> SUZUKI, Toshiharu et al.

<120> MARKER PEPTIDE FOR ALZHEIMER'S DISEASE

<130> 3749-0112PUS1

<140> 10577008

<141> 2006-08-07

<150> PCT/JP2004/016209

<151> 2004-11-01

<150> JP 2003/375363

<151> 2003-11-05

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 971

<212> PRT

<213> human

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Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile Val Thr Glu
35 40 45

Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile Ala Leu Asp Lys
50 55 60

Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile Cys Gly Phe Lys Ile His
65 70 75 80

Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr Gly
85 90 95

Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu Gln Lys
100 105 110

Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys Gly Pro Asp
115 120 125

Gly Thr Asn Val Lys Lys Ser His Lys Ala Thr Val His Ile Gln Val
130 135 140

Asn Asp Val Asn Glu Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys
145 150 155 160

Ala Thr Val Ile Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu
165 170 175

Ala Val Asp Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr
180 185 190

Glu Ile Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr
195 200 205

Ile Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys
210 215 220

Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu Asp
225 230 235 240

Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly Trp Gln
245 250 255

Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly Ala Leu Ala
260 265 270

Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu Pro Val Ala Ser
275 280 285

Val Gln Ala Thr Val Glu Leu Glu Thr Ser His Ile Gly Lys Gly Cys
290 295 300

Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu His Arg Leu Cys Gly Ala
305 310 315 320

Ala Ala Gly Thr Ala Glu Leu Leu Pro Ser Pro Ser Gly Ser Leu Asn
325 330 335

Trp Thr Met Gly Leu Pro Thr Asp Asn Gly His Asp Ser Asp Gln Val

340

345

350

Phe Glu Phe Asn Gly Thr Gln Ala Val Arg Ile Pro Asp Gly Val Val
 355 360 365

Ser Val Ser Pro Lys Glu Pro Phe Thr Ile Ser Val Trp Met Arg His
 370 375 380

Gly Pro Phe Gly Arg Lys Lys Glu Thr Ile Leu Cys Ser Ser Asp Lys
 385 390 395 400

Thr Asp Met Asn Arg His His Tyr Ser Leu Tyr Val His Gly Cys Arg
 405 410 415

Leu Ile Phe Leu Phe Arg Gln Asp Pro Ser Glu Glu Lys Lys Tyr Arg
 420 425 430

Pro Ala Glu Phe His Trp Lys Leu Asn Gln Val Cys Asp Glu Glu Trp
 435 440 445

His His Tyr Val Leu Asn Val Glu Phe Pro Ser Val Thr Leu Tyr Val
 450 455 460

Asp Gly Thr Ser His Glu Pro Phe Ser Val Thr Glu Asp Tyr Pro Leu
 465 470 475 480

His Pro Ser Lys Ile Glu Thr Gln Leu Val Val Gly Ala Cys Trp Gln
 485 490 495

Glu Phe Ser Gly Val Glu Asn Asp Asn Glu Thr Glu Pro Val Thr Val
 500 505 510

Ala Ser Ala Gly Gly Asp Leu His Met Thr Gln Phe Phe Arg Gly Asn
 515 520 525

Leu Ala Gly Leu Thr Leu Arg Ser Gly Lys Leu Ala Asp Lys Lys Val
 530 535 540

Ile Asp Cys Leu Tyr Thr Cys Lys Glu Gly Leu Asp Leu Gln Val Leu
 545 550 555 560

Glu Asp Ser Gly Arg Gly Val Gln Ile Gln Ala His Pro Ser Gln Leu
 565 570 575

Val Leu Thr Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met
580 585 590

Gln His Ile Ser Tyr Leu Asn Ser Arg Gln Phe Pro Thr Pro Gly Ile
595 600 605

Arg Arg Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr
610 615 620

Cys Ile Ser Val Pro Pro Val Asp Gly Tyr Val Met Val Leu Gln Pro
625 630 635 640

Glu Glu Pro Lys Ile Ser Leu Ser Gly Val His His Phe Ala Arg Ala
645 650 655

Ala Ser Glu Phe Glu Ser Ser Glu Gly Val Phe Leu Phe Pro Glu Leu
660 665 670

Arg Ile Ile Ser Thr Ile Thr Arg Glu Val Glu Pro Glu Gly Asp Gly
675 680 685

Ala Glu Asp Pro Thr Val Gln Glu Ser Leu Val Ser Glu Glu Ile Val
690 695 700

His Asp Leu Asp Thr Cys Glu Val Thr Val Glu Gly Glu Glu Leu Asn
705 710 715 720

His Glu Gln Glu Ser Leu Glu Val Asp Met Ala Arg Leu Gln Gln Lys
725 730 735

Gly Ile Glu Val Ser Ser Ser Glu Leu Gly Met Thr Phe Thr Gly Val
740 745 750

Asp Thr Met Ala Ser Tyr Glu Glu Val Leu His Leu Leu Arg Tyr Arg
755 760 765

Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile Cys
770 775 780

Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val Glu Val
785 790 795 800

Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn His Met Ala
805 810 815

Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser Phe Val Asp Leu
820 825 830

Ser Gly His Asn Leu Ala Asn Pro His Pro Phe Ala Val Val Pro Ser
835 840 845

Thr Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met
850 855 860

Ile Ile Leu Gly Val Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met
865 870 875 880

Arg Asp Gln Asp Thr Gly Lys Glu Asn Glu Met Asp Trp Asp Asp Ser
885 890 895

Ala Leu Thr Ile Thr Val Asn Pro Met Glu Thr Tyr Glu Asp Gln His
900 905 910

Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp
915 920 925

Gly Glu Glu Glu Asp Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu
930 935 940

Glu Glu Glu Gly Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln
945 950 955 960

Gln Leu Glu Trp Asp Asp Ser Thr Leu Ser Tyr
965 970

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<212> PRT
<213> human

<400> 2

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Val Glu Ala Leu Leu Thr Gly Ala Ser Ser Pro Leu Pro Gly Val Gly

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25

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Pro Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu Tyr Gln Gly Ile
 35 40 45

Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro Pro Leu Phe Ala
 50 55 60

Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu Ile Cys Gly Phe
 65 70 75 80

Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val Ile Leu Asp Lys
 85 90 95

Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro Val Asp Cys Glu
 100 105 110

Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr Asp Cys Gly Glu
 115 120 125

Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys Ala Thr Val His
 130 135 140

Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val Phe Val Glu Arg
 145 150 155 160

Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr Asp Arg Ile Leu
 165 170 175

Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln Tyr Ser Gln Ile
 180 185 190

Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe Leu Ile Asp Asn
 195 200 205

Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr Ser Gly Glu Arg
 210 215 220

Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala
 225 230 235 240

Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro Thr Cys Lys Pro
 245 250 255

Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala Pro Gly Ala Gly
260 265 270

Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr Cys Asp Glu Pro
275 280 285

Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr Ser His Val Ala
290 295 300

Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala Leu Arg Lys Leu
305 310 315 320

Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro Met Pro Gly Pro
325 330 335

Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr Ser Gln Asp Ser
340 345 350

Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val Gln Val Pro Leu
355 360 365

Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp Ser Leu Ser Asp
370 375 380

His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val Thr Pro Asn Lys
385 390 395 400

Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr Val Gln Asn Glu
405 410 415

Asp Gly Phe Ser His Tyr Ser Leu Thr Val His Gly Cys Arg Ile Ala
420 425 430

Phe Leu Tyr Trp Pro Leu Leu Glu Ser Ala Arg Pro Val Lys Phe Leu
435 440 445

Trp Lys Leu Glu Gln Val Cys Asp Asp Glu Trp His His Tyr Ala Leu
450 455 460

Asn Leu Glu Phe Pro Thr Val Thr Leu Tyr Thr Asp Gly Ile Ser Phe
465 470 475 480

Asp	Pro	Ala	Leu	Ile	His	Asp	Asn	Gly	Leu	Ile	His	Pro	Pro	Arg	Arg	485	490	495
Glu	Pro	Ala	Leu	Met	Ile	Gly	Ala	Cys	Trp	Thr	Glu	Glu	Lys	Asn	Lys	500	505	510
Glu	Lys	Glu	Lys	Gly	Asp	Asn	Ser	Thr	Asp	Thr	Thr	Gln	Gly	Asp	Pro	515	520	525
Leu	Ser	Ile	His	His	Tyr	Phe	His	Gly	Tyr	Leu	Ala	Gly	Phe	Ser	Val	530	535	540
Arg	Ser	Gly	Arg	Leu	Glu	Ser	Arg	Glu	Val	Ile	Glu	Cys	Leu	Tyr	Ala	545	550	555
Cys	Arg	Glu	Gly	Leu	Asp	Tyr	Arg	Asp	Phe	Glu	Ser	Leu	Gly	Lys	Gly	565	570	575
Met	Lys	Val	His	Val	Asn	Pro	Ser	Gln	Ser	Leu	Leu	Thr	Leu	Glu	Gly	580	585	590
Asp	Asp	Val	Glu	Thr	Phe	Asn	His	Ala	Leu	Gln	His	Val	Ala	Tyr	Met	595	600	605
Asn	Thr	Leu	Arg	Phe	Ala	Thr	Pro	Gly	Val	Arg	Pro	Leu	Arg	Leu	Thr	610	615	620
Thr	Ala	Val	Lys	Cys	Phe	Ser	Glu	Glu	Ser	Cys	Val	Ser	Ile	Pro	Glu	625	630	635
Val	Glu	Gly	Tyr	Val	Val	Val	Leu	Gln	Pro	Asp	Ala	Pro	Gln	Ile	Leu	645	650	655
Leu	Ser	Gly	Thr	Ala	His	Phe	Ala	Arg	Pro	Ala	Val	Asp	Phe	Glu	Gly	660	665	670
Thr	Asn	Gly	Val	Pro	Leu	Phe	Pro	Asp	Leu	Gln	Ile	Thr	Cys	Ser	Ile	675	680	685
Ser	His	Gln	Val	Glu	Ala	Lys	Lys	Asp	Glu	Ser	Trp	Gln	Gly	Thr	Val	690	700	

Thr Asp Thr Arg Met Ser Asp Glu Ile Val His Asn Leu Asp Gly Cys
705 710 715 720

Glu Ile Ser Leu Val Gly Asp Asp Leu Asp Pro Glu Arg Glu Ser Leu
725 730 735

Leu Leu Asp Thr Thr Ser Leu Gln Gln Arg Gly Leu Glu Leu Thr Asn
740 745 750

Thr Ser Ala Tyr Leu Thr Ile Ala Gly Val Glu Ser Ile Thr Val Tyr
755 760 765

Glu Glu Ile Leu Arg Gln Ala Arg Tyr Arg Leu Arg His Gly Ala Ala
770 775 780

Leu Tyr Thr Arg Lys Phe Arg Leu Ser Cys Ser Glu Met Asn Gly Arg
785 790 795 800

Tyr Ser Ser Asn Glu Phe Ile Val Glu Val Asn Val Leu His Ser Met
805 810 815

Asn Arg Val Ala His Pro Ser His Val Leu Ser Ser Gln Gln Phe Leu
820 825 830

His Arg Gly His Gln Pro Pro Pro Glu Met Ala Gly His Ser Leu Ala
835 840 845

Ser Ser His Arg Asn Ser Met Ile Pro Ser Ala Ala Thr Leu Ile Ile
850 855 860

Val Val Cys Val Gly Phe Leu Val Leu Met Val Val Leu Gly Leu Val
865 870 875 880

Arg Ile His Ser Leu His Arg Arg Val Ser Gly Ala Gly Gly Pro Pro
885 890 895

Gly Ala Ser Ser Asp Pro Lys Asp Pro Asp Leu Phe Trp Asp Asp Ser
900 905 910

Ala Leu Thr Ile Ile Val Asn Pro Met Glu Ser Tyr Gln Asn Arg Gln
915 920 925

Ser Cys Val Thr Gly Ala Val Gly Gly Gln Gln Glu Asp Glu Asp Ser

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935

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Ser Asp Ser Glu Val Ala Asp Ser Pro Ser Ser Asp Glu Arg Arg Ile
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Ile Glu Thr Pro Pro His Arg Tyr
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Val Gly Ser Gly Ser Gly Gly Gly Gly Asp Ser Arg Gln Arg Arg Leu
20 25 30

Leu Ala Ala Lys Val Asn Lys His Lys Pro Trp Ile Glu Thr Ser Tyr
35 40 45

His Gly Val Ile Thr Glu Asn Asn Asp Thr Val Ile Leu Asp Pro Pro
50 55 60

Leu Val Ala Leu Asp Lys Asp Ala Pro Val Pro Phe Ala Gly Glu Ile
65 70 75 80

Cys Ala Phe Lys Ile His Gly Gln Glu Leu Pro Phe Glu Al